

STRENGTHS AND WEAKNESSES OF METHODS OF INCORPORATING GENOMICS INTO GENETIC EVALUATION

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Neraska 36538, Champion Bull Aberdeen 1915
Grand Champion (as steer) Smithfield 1916

HISTORICAL COMMENTARY

- Genomic Selection relative to National Cattle Evaluation is the only thing a 34 year old has historical knowledge of.

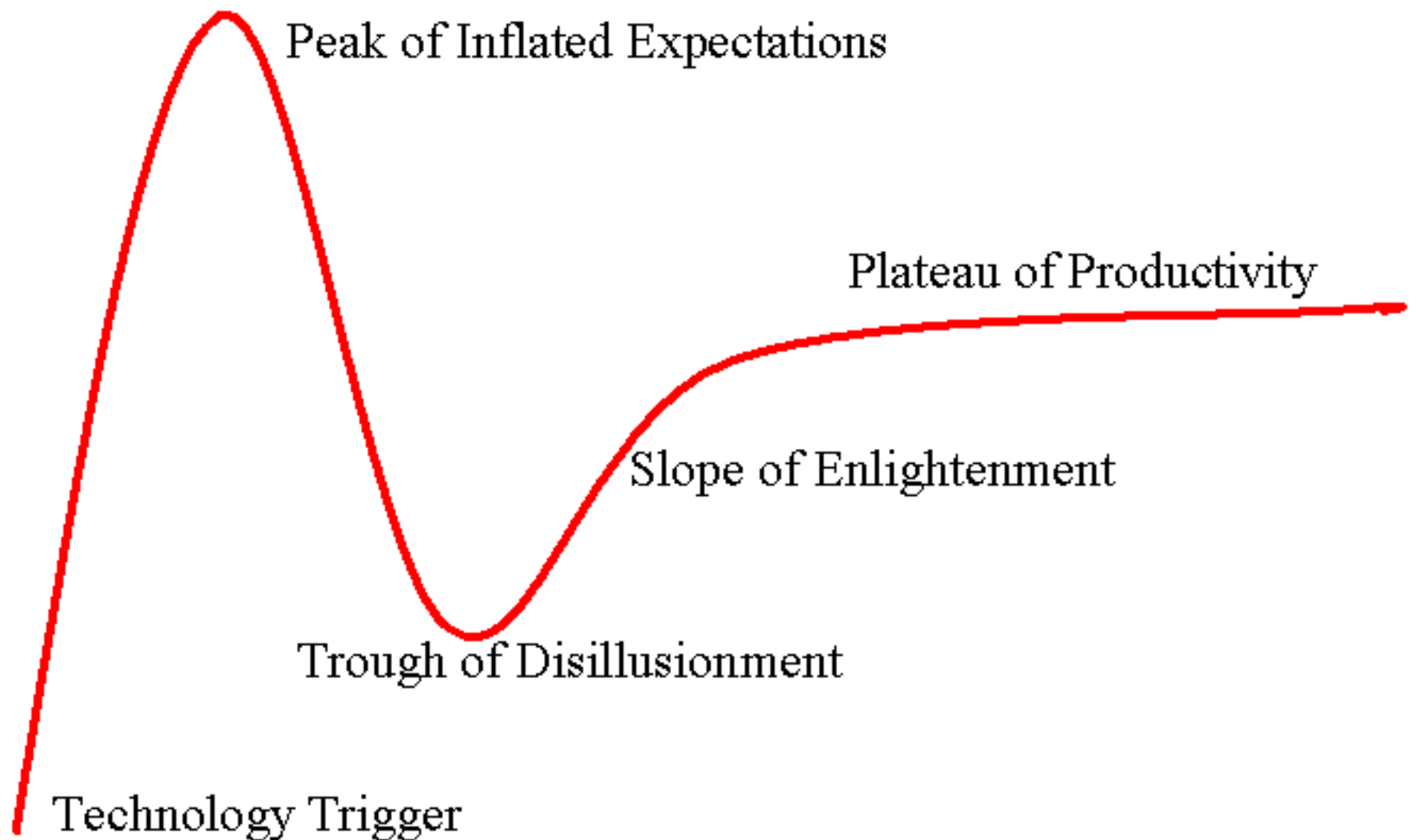
PAST STATUS=CONFUSION

	CE	BW	WW	YW	MCE	MM	MWW
Adj.		90	700	1320			
Ratio		101	107				
EPD	9	-1.0	25	49	3	11	23
Acc	.29	.37	.30	.27	.18	.19	.23

	YG	Marb	BF	REA
Adj.		4.65%	.23	12.5
Ratio		106	100	95
EPD	.21	.44	.05	-.39
Acc	.32	.31	.33	.34

REA	TEND	MARB
7	6	8

Gartner Hype Cycle

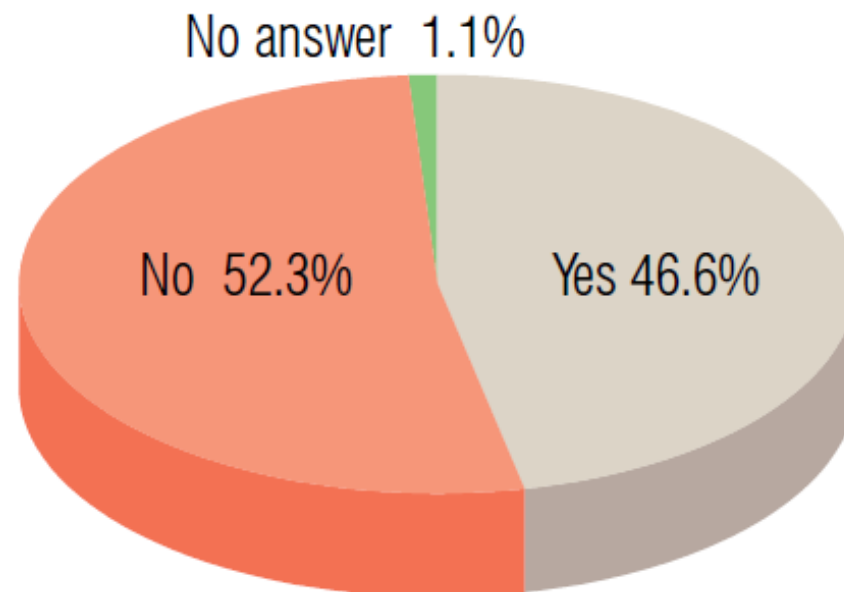


MERGER OF ALL INFORMATION

- American Simmental Association
 - Tenderness
- American Angus Association
 - “Correlated Trait Approach”—Kachman (2008)
 - Made widely known by MacNeil (2010)

MARCH 1, 2010 BEEF MAGAZINE SURVEY

Do you feel like you have a good understanding of the genomic (DNA) information being offered by some seedstock suppliers?



ADOPTION OF GENOMIC PREDICTIONS

- Efficacy of this technology is not binary
- The adoption of this must be centered on the gain in EPD accuracy
 - This is related to the proportion of genetic variation explained by a Molecular Breeding Values (MBV; Result of DNA Test)
 - % GV = squared genetic correlation

TREMENDOUS FIRST STEP

- Simplification
- Conceptually appealing
- Fit current NCE
- Information benefits more than just the genotyped animal
- Multiple companies increases complexity
- Assumes MBV predicts all animals equally as well

PROCESS



$$MBV = \sum_{i=1}^s \hat{a}_i x_i \hat{b}_i$$

PARADIGM

- Companies develop prediction equations (do training)
- Brought technology to market in a useable form
- Hold IP
- Training sets were “unknown” and not as dynamic



LEVERAGING INFORMATION

- Could other breeds make use of the Angus investment in genomics
 - Was this transferable across breeds?



AMERICAN
Simmental
ASSOCIATION

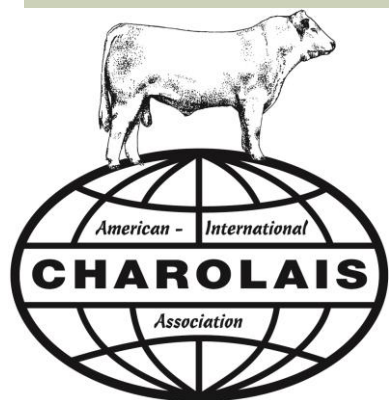
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National Colorado State University-Cornell University-University of Georgia
Beef Cattle Evaluation
Consortium



Building Better Beef...
Red Angus



ANGUS
THE BUSINESS BREED

INITIAL EVALUATION EFFORTS

- 384 SNP for Weaning weight
- Training on MARC Cycle VII
 - 3,328 calves
 - 192 SNP discovered here
 - 192 from Igenity
 - After QC 255 (diagnostic=159)
 - Some of the most valuable SNP excluded

WTP-POPULATION

- Seven major U.S. beef breeds
 - Angus, Hereford, Red Angus, Simmental, Limousin, Charolais, Gelbvieh
- Total of 3,500 2009 born bulls calves genotyped
- Over 19,000 DNA samples collected

BREED CONTRIBUTION TO TRAINING

Breed	Average Contribution
Angus	26
Hereford	19
Red Angus	6.5
Simmental	6.5
Charolais	6.5
Gelbvieh	6.5
Limousin	6.5

WTP-RESULTS

(Spangler et al., 2011)

Breed	Weaning Weight Direct		Weaning Weight Maternal	
	WW MBV	PWG MBV	WW MBV	PWG MBV
Angus	0.00 (0.10)	0.14 (0.10)	0.00 (0.17)	-0.04 (0.17)
Red Angus	0.10 (0.10)	0.35 (0.09)	0.02 (0.16)	-0.18 (0.15)
Charolais	0.28 (0.15)	-0.06 (0.17)	0.14 (0.20)	0.05 (0.22)
Gelbvieh	0.25 (0.13)	0.25 (0.12)	-0.22 (0.22)	-0.03 (0.22)
Hereford	0.20 (0.20)	0.29 (0.20)	0.06 (0.28)	-0.06 (0.29)
Limousin	0.24 (0.12)	0.18 (0.12)	-0.53 (0.22)	-0.08 (0.23)
Simmental	-0.05 (0.08)	-0.06 (0.08)	0.22 (0.13)	0.19 (0.12)

BREED SPECIFICITY

(Kachman et al., 2013)

	Weaning weight MBV		
Breed	Angus	Hereford	Limousin
Angus	0.36±0.07	0.14±0.08	-0.06±0.08
Red Angus	0.16±0.16	0.09±0.16	0.25±0.16
Hereford	0.04±0.21	0.42±0.18	0.27±0.21
Limousin	0.02±0.09	0.23±0.09	0.40±0.08

ACROSS BREED PREDICTIONS FOR REA

- If breeds are contained in training, predictions work well
- If not, correlations decrease

	Pooled Training (AN, SM, HH, LM)
AN	0.43 (0.07)
SM	0.34 (0.09)
HH	0.33 (0.08)
GV	0.17 (0.11)

OTHER BREEDS MADE AN INVESTMENT

- Existing projects helped as a starting platform
 - 2,000 Bull Project
 - University of Missouri
 - Weight Trait Project

PARADIGM SHIFT

- **Flexibility**
 - “Control your own destiny”
 - Can alter integration methods
- **Other breeds sought help from the NBCEC (Garrick) in training**

CURRENT STATUS (GARRICK 2013)

Breed	50K Samples	Deployed GEPD
Shorthorn	450	No
Hereford	5,557	Yes
Red Angus	1,794	Yes
Simmental	5,240	Yes
Brangus	1,418	No
Angus	11,334	Yes
Limousin	3,275	Yes
Gelbvieh	1,440	Nearing
Charolais	934	No
Maine Anjou	948	Nearing

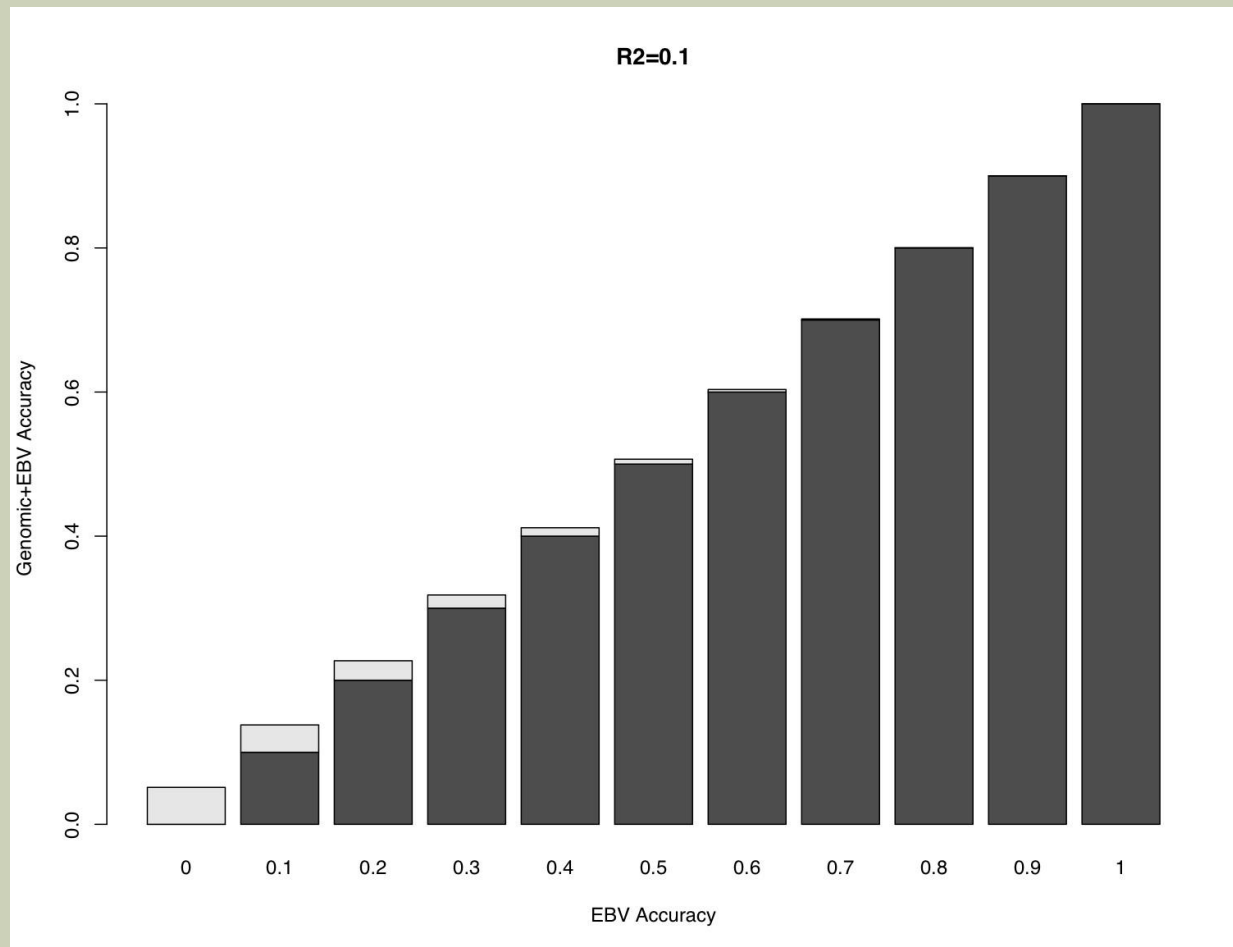
BREEDS WITH GENOMIC-EPD RELEASED OR PROTOTYPE

- Angus—Neogen and Zoetis
- Hereford--NBCEC
- Simmental--NBCEC
- Red Angus—NBCEC and Zoetis
- Limousin
- Gelbvieh
- Brahman (Tenderness)—Zoetis

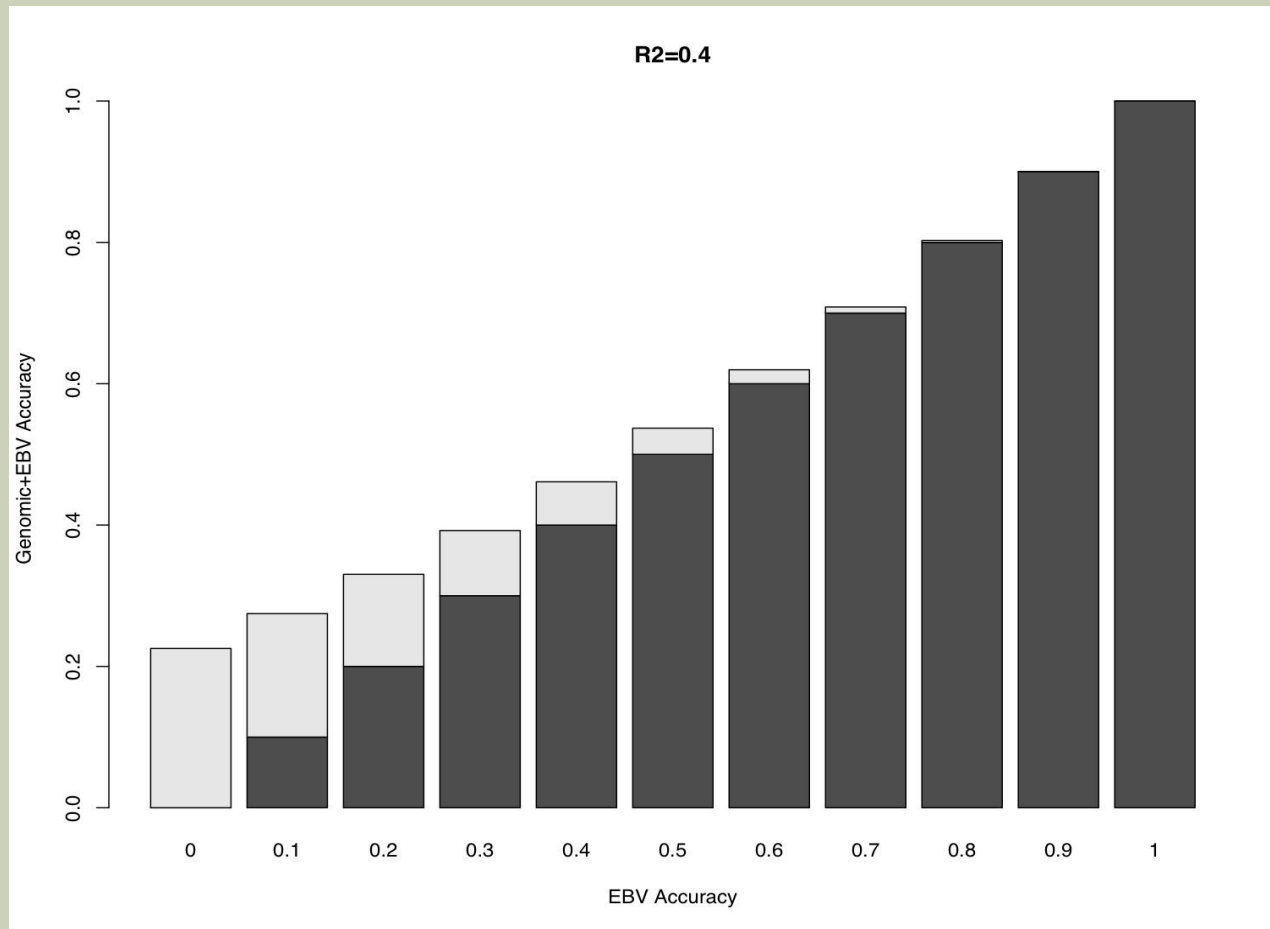


THIS IS A SUCCESS STORY!

IMPACT ON ACCURACY--%GV=10%



IMPACT ON ACCURACY--%GV=40%



“BLENDING”

- Post evaluation indexing of EPD and MBV
- Benefits only genotyped animals
- Simplicity
- Fits within framework of NCE
- Must “blend” correctly...

THRESHOLD TRAITS ARE DIFFERENT

(Kachman and Spangler, 2013)

Trait	N	NBCEC Prediction Observed Scale Genetic Correlation	NBCEC Prediction Underlying Scale Genetic Correlation
Calving Ease Maternal	170	0.458	0.679 (0.058)
Calving Ease Direct	176	0.479	0.588 (0.067)
Heifer Pregnancy	64	0.616	0.610 (0.124)
Stayability	104	0.801	0.787 (0.118)

CURRENT METHODS

- All different themes on the Two-Step Approach
- Why?
 - Method of inclusion dependent on NCE provider (and software)
 - Initially, genotypes were unavailable
 - Fear of computational (and storage) demands
 - As number of genotyped animals grows, SS-BLUP can become computationally expensive
 - Most NCE software is “historic” and not flexible

VARIABLE ACCURACY

- American Simmental Association attempted this
- Logical philosophy
- Relationship differences between target animals and training animals
 - Relationship also impacted by accuracy of training animal's EPD

OTHER UNACCOUNTED FOR BIAS

- Training sets represent a selected subset
 - Problem erodes overtime with more genotyped animals and dynamic training
 - Problems likely most notable for traits that are hallmarks of the breed

CHANGES TO TECHNOLOGY PLATFORMS

NEW ASSAYS

- Bovine SNP50 (50K) had been the backbone
- GGP-LD (~9K; 8K in common with 50K)
- GGP-HD (~80K; 28K in common with 50K)
- HD (~770K)



700K RESULTS: MILK VOLUME

50k	F Fries	F Jers	F HFxJ
Friesians	0.69	0.47	0.58
Jerseys	0.45	0.56	0.47
HFxJ	0.66	0.43	0.60

700k	F Fries	F Jers	F HFxJ
Friesians	0.70	0.18	0.59
Jerseys	0.39	0.59	0.50
HFxJ	0.65	0.43	0.62

DIFFERENT WAY TO LOOK AT IT

- Using knowledge of variants to inform marker selection

Correlation	Rex Ranch (BW)
50K panel	.10
770K panel	.32

MOVING FORWARD

- We have made tremendous progress
- More work to do
- Evolutions in:
 - Methodology
 - NCE platforms
 - Cannot continue to make genomics “fit”
 - Opportunity to rebuild instead of patch
 - Continuous NCE
 - Who does training
 - Understanding (adoption)
 - Confusion around GE-EPD is an artifact of never having understood EPD

UNDERSTANDING

- Collection of phenotypes
 - Retraining efforts
 - Increase in accuracy above what genomics can do

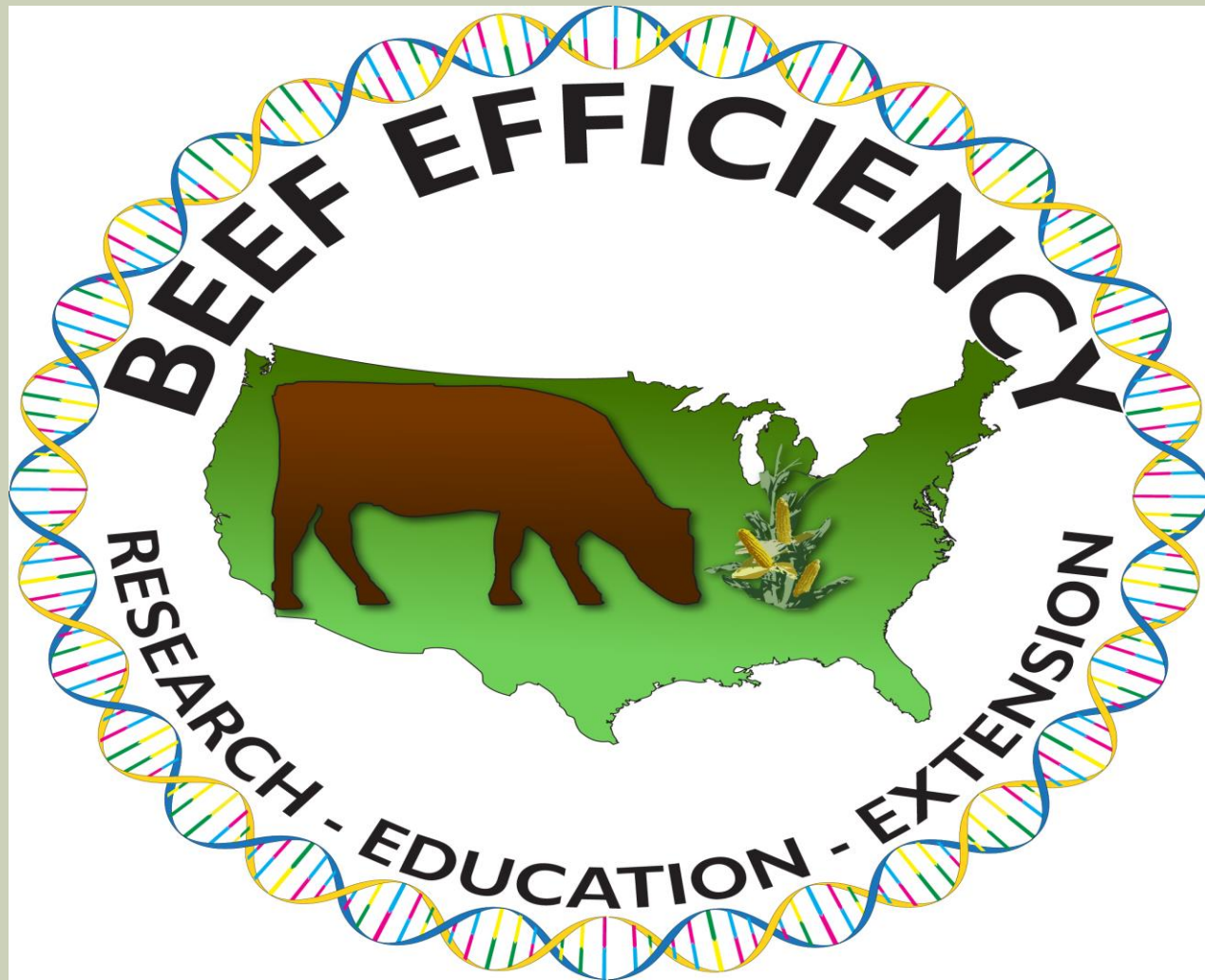
ACCURACY

Table 1. Approximate number of progeny needed to reach accuracy levels (true (r) and the BIF standard) for three heritabilities (h^2).

<u>Accuracy</u>		<u>Heritability Levels</u>		
r	BIF	h^2 (0.1)	h^2 (0.3)	h^2 (0.5)
0.1	0.01	1	1	1
0.2	0.02	2	1	1
0.3	0.05	4	2	1
0.4	0.08	8	3	2
0.5	0.13	13	5	3
0.6	0.2	22	7	4
0.7	0.29	38	12	7
0.8	0.4	70	22	13
0.9	0.56	167	53	30
0.999	0.99	3800	1225	700

MBV BIF ACCURACY

Genetic Correlation	% GV	BIF Accuracy
0.1	1	0.005
0.2	4	0.020
0.3	9	0.046
0.4	16	0.083
0.5	25	0.132
0.6	36	0.2
0.7	49	0.286



WWW.BEEFEFFICIENCY.ORG

Cattle Production & Genotyping

Breed	SNP50	HD	#Animals	#SNPs ¹	2013 Animals ²	2013 Projected ³	Total Animals
Angus	1,093	573	1,666	747,473	326		1,992
Charolais		24	24	N/A	13		37
Charolais x Ang						450	450
Commercial Crossbred					212		212
Gelbvieh x Ang		317	317	N/A			317
Hereford	368	502	870	684,458	275	200	1,345
Limousin		39	39	568,501	45	45	129
Normande					3		3
Pied x Ang x Simm					236		236
Red Angus		155	155	694,847	94		249
Red Angus x Ang		158	158	N/A			158
Simm x Ang	2,251	467	2,718	690,184		909	3,627
Wagyu	27	19	46	N/A		120	166
Total	3,739	2,254	5,993		1,204	1,724	8,921

¹Imputed using Beagle

²SNP50 genotyped

³Doesn't include data swap with TEASUG, Canadian Feed Efficiency Consortium or Genus collaboration

Heritabilities

Breed	DMI (lb)			MMWT (lb ^{0.75})			ADG (lb/d)			RFI (lb/d)		
	VA	VE	h ²	VA	VE	h ²	VA	VE	h ²	VA	VE	h ²
Hereford	3.2	4.6	0.41	79	78	0.50	0.09	0.23	0.27	1.60	1.90	0.45
USMARC	1.9	3.4	0.35	84	97	0.47	0.07	0.16	0.30	0.91	0.94	0.49
Simmental x Angus	1.4	3.7	0.27	28	36	0.48	0.04	0.13	0.23	0.96	2.02	0.32
Angus	4.1	7.5	0.35	125	130	0.49	0.06	0.24	0.19	1.30	4.80	0.21

- Additive genetic variance tends to be lower in composite animals
- Larger residual variance for Angus (and lower heritability) probably reflects feeding at two different locations using Calan Gates versus GrowSafe systems

HD (770K) RESULTS FOR ANGUS AND HEREFORD

- US Consortium for the Genetic Improvement of Feed Efficiency in Beef Cattle

Breed	Trait	S_G^2 (lb ²)	S_E^2 (lb ²)	h^2	Largest QTL % S_G^2	Largest 10 QTL % S_G^2
Angus (N=1579)	DMI	4.12	7.51	0.35	10.39	21.02
	RFI	1.30	4.76	0.21	2.21	9.11
Hereford (N=847)	DMI	3.23	4.57	0.41	4.33	12.58
	RFI	1.57	1.94	0.45	1.57	8.04

?

MOVING FORWARD-NOVEL TRAITS

- Training will occur on phenotypes (not deregressed EBV)
- Expense of data collection could reasonably lead to highly selected training sets
- Inference becomes challenging
- Bias could become a real issue

SUMMARY

- Phenotypes are still critical to collect
- Methods for lower cost genotyping are evolving
- Breeds must build training populations to capitalize
- Genomic information has the potential to increase accuracy
 - Proportional to %GV
 - Impacts inversely related to prior EPD accuracy
- Adoption in the beef industry is problematic
 - ~30% of cows in herds with < 50 cows
 - Adoption must start at nucleus level
 - BEEF INDUSTRY HAS TO BECOME MORE SOPHISTICATED!

THANK YOU

- <http://beef.unl.edu>
- www.nbcec.org
- www.beefefficiency.org

